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A Mathematical Model on the Spread of COVID-19

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Abstract

In this paper, a nonlinear mathematical model of COVID-19 was formulated. We proposed a SEIQR model using a system of ordinary differential equations. COVID-19 free equilibrium and endemic equilibrium points of the model are obtained. The next-generation matrix investigates a basic reproduction number of the model. The stability analysis of the model equilibrium points was investigated using basic reproduction numbers. The results show that the disease-free equilibrium of the COVID-19 model is stable if the primary reproduction number is less than unity and unstable if the basic reproduction number is greater than unity. Sensitivity analysis was rigorously analyzed. Finally, numerical simulations are presented to illustrate the results.

Keywords: COVID-19, Pandemic, Reproduction number, Stability analysis, Equilibrium point.

1 | Introduction

Coronaviruses are a massive circle of relatives of viruses that could cause contamination in human beings that acknowledged to purpose respiration infections ranging from the now not unusual place bloodless to extra excessive illnesses together with Middle East Respiratory Syndrome (MERS) and Severe Acute Respiratory Syndrome (SARS). A novel Coronavirus, formerly precise 2019-nCoV, became recognized because of the purpose of a cluster of Pneumonia instances in Wuhan, a town inside the Hubei Province of China, on the cease of 2019. It eventually unfolds at some stage in China and elsewhere, turning into an international fitness emergency. In February 2020, the World Health Organization (WHO) declared COVID-19, which stands for Coronavirus ailment 2019, an international pandemic [1].

According to the WHO report, all over the world, as of December 29, 2020, there have been 79,931,215 confirmed cases of COVID-19, including 1,765,265 deaths, reported to WHO [2]. Investigations are still ongoing to assess the source of the disease, the mode or modes of transmission, and the extent of infection. Currently, the available evidence of the emerging Coronavirus and past experiences with other Coronavirus

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(MERS and SARS virus) and other respiratory symptoms viruses (such as bird flu) indicate the possibility of the new virus transmission from an animal source [3]–[6].

The main transmission routes of the Coronavirus are through coughing, sneezing, contacting infected people, or touching items or surfaces contaminated with fecal traces [4]. In order to combat this pandemic, different preventive measures are recommended, such as avoiding close contact with sick people, avoiding touching the eyes, nose, and mouth with unwashed hands, washing hands often with soap and water for at least 20 seconds, using an alcohol-based hand sanitizer containing at least 60% alcohol when soap and water are not available.

Developing a mathematical model for the Coronavirus (COVID-19) is of great importance as it helps explain the extent of the disease, considering that it is an invisible and infectious virus. Based on this mathematical model, we can judge whether approved measures such as quarantine are sufficient to limit the spread of the virus.

Many studies and research of mathematical models can be used to analyze the spread of the Coronavirus [4], [7]–[11]. In [9], the SEIR version concerning the susceptible, the exposed, the infected, and the recovered people becomes considered. Results after simulating diverse eventualities imply that dismissing social distancing and hygiene measures could have devastating consequences for the human population. In [7], a mathematical model was developed to integrate asymptomatic people and the isolation of infected persons, the quarantine of contacting people, and the home containment of all population strategies. It is established by theoretical investigation and illustrated by simulations that containment is fundamental to prevent the disease from spreading without a vaccine. In [11], the SEIRU version concerning the susceptible, the exposed, the infected, the quarantined, and the recovered people changed into consideration. It is expected that there's a hazard of a decline in secondary infections while all precautionary measures are determined globally.

We will propose a mathematical model defining and describing the spread of the new Coronavirus (COVID-19). Compartmental models played a central role during the development of epidemiology modeling in the population. The majority of cases of (COVID-19) spread from human-to-human connection. In this work, we adopt the basic Susceptible-Exposed-Infected-Recovered (SEIR) model and extend it into SEIQR, where the quarantined Q class is added.

2|Model Description and Analysis

We propose a continuous model SEIQR to describe the interaction within a population where the disease COVID-19 exists. We consider the cases of (the COVID-19) virus spread from a human-to-human connection. The model subdivides the entire human population period at time t denoted as $N(t)$ into susceptible $S(t)$, exposed $E(t)$, Infected people with symptoms and carriers of the virus $I(t)$, Quarantined Infected (Hospitalized cases) $Q(t)$ and the recovered as R(t). The total number of the human population at time t is given by $N(t) = S(t) + E(t) + I(t) + Q(t) + R(t)$. Individuals are recruited at π is the new birth rate in the susceptible human population, β_1 represents the transmission coefficient from susceptible individuals to exposure due to the movement and contact that occur among them, β_2 represents the transmission coefficient from susceptible individuals infected individuals with symptoms and carriers of the virus due to the movement and contact among them, μ represents the natural death rate in all compartments, σ represents the progression rate from E to either I or R. The exposed individuals become infectious and join the infected compartment at $\delta\sigma$, and the remaining proportion of these exposed individuals develop natural immunity and recover from the disease at $(1-\delta)\sigma$ and ω is the transmission coefficient of the infected people with symptoms and carriers of the virus to the quarantined infected (hospitalized cases) γ is the transmission coefficient of the quarantined infected (hospitalized cases) to the recovered cases. The recovered individuals become again susceptible to the disease at a rate of θ, α_1 and α_2 respectively, representing the death rate of the infected population and the death rate of the quarantined infected (hospitalized cases) population due to COVID-19 infection. Based on the above state variables and model assumptions, we consider the following system of five nonlinear differential equations:

$$\frac{dS}{dt} = \pi + \theta R - \mu S - \frac{\beta_1 SE + \beta_2 SI}{N}, \quad (1)$$

$$\frac{dE}{dt} = \frac{\beta_1 SE + \beta_2 SI}{N} - (\mu + \sigma)E, \quad (2)$$

$$\frac{dI}{dt} = \delta\sigma E - (\mu + \alpha_1 + \omega)I, \quad (3)$$

$$\frac{dQ}{dt} = \omega I - (\mu + \alpha_2 + \gamma)Q, \quad (4)$$

$$\frac{dR}{dt} = (1 - \delta)\sigma E + \gamma Q - (\mu + \theta)R, \quad (5)$$

with the initial condition $S(0) > 0, E(0) \geq 0, I(0) \geq 0, Q(0) \geq 0$ and $R(0) \geq 0$.

2.1 | Basic Properties of the Model

2.1.1 | Invariant region

In this subsection, we determine a region in which the solution of *Models (1)-(5)* is bounded. For this model, the total population is $N(t) = S(t) + E(t) + I(t) + Q(t) + R(t)$. Then, differentiating $N(t)$ with respect to time, we obtain

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dE}{dt} + \frac{dI}{dt} + \frac{dQ}{dt} + \frac{dR}{dt} = \pi - \alpha_1 I - \alpha_2 Q - \mu N.$$

If there is no death due to the disease, we get

$$\frac{dN}{dt} \leq \pi - \mu N.$$

After evaluating, we obtain

$$N(t) \leq \left(N(0) - \frac{\pi}{\mu}\right) e^{-\mu t} + \frac{\pi}{\mu}.$$

As $t \to \infty$, we obtain $\Omega = \left\{(S, E, I, Q, R) \in R_+^5 : 0 < N \leq \frac{\pi}{\mu}\right\}$.

Therefore, the model equation is well-posed epidemiologically and mathematically. Hence, it is sufficient to study the dynamics of the basic model in the region Ω.

2.1.2 | Positivity of solutions

Theorem 1. If $S(0) > 0, E(0) \geq 0, I(0) \geq 0, Q(0) \geq 0, R(0) \geq 0$ are positive in the feasible set Ω, then the solution set $(S(t), E(t), I(t), Q(t), R(t))$ of *Systems (1)-(5)* is positive for all $t \geq 0$.

Proof: from the first equation of the system

$$\frac{dS}{dt} = \pi + \theta R - \mu S - \frac{\beta_1 SE + \beta_2 SI}{N}.$$

$$\frac{dS}{dt} + \left(\mu + \frac{\beta_1 E + \beta_2 I}{N}\right) S = \pi + \theta R.$$

This equation is a first-order linear ordinary differential equation. Whose integrating factor

$$IF = e^{\int_0^t \left(\mu + \frac{\beta_1 E + \beta_2 I}{N}\right) d\tau}.$$

Now, multiplying the differential Equation by its integrating factor, we obtain

$$e^{\int_0^t \left(\mu + \frac{\beta_1 E + \beta_2 I}{N}\right) d\tau} \frac{dS}{dt} + e^{\int_0^t \left(\mu + \frac{\beta_1 E + \beta_2 I}{N}\right) d\tau} \left(\mu + \frac{\beta_1 E + \beta_2 I}{N}\right) S = e^{\int_0^t \left(\mu + \frac{\beta_1 E + \beta_2 I}{N}\right) d\tau} (\pi + \theta R).$$

$$d\left(S e^{\int_0^t \left(\mu + \frac{\beta_1 E + \beta_2 I}{N}\right) d\tau}\right) = e^{\int_0^t \left(\mu + \frac{\beta_1 E + \beta_2 I}{N}\right) d\tau} (\pi + \theta R) dt.$$

Integrate both sides in the interval $[0, t]$

$$\int_0^t d\left(Se^{\int_0^t\left(\mu+\frac{\beta_1 E+\beta_2 I}{N}\right)d\tau}\right) = \int_0^t e^{\int_0^t\left(\mu+\frac{\beta_1 E+\beta_2 I}{N}\right)d\tau}(\pi+\theta R)\,d\tau.$$

$$S(t)e^{\int_0^t\left(\mu+\frac{\beta_1 E+\beta_2 I}{N}\right)d\tau} - S(0) = \int_0^t e^{\int_0^t\left(\mu+\frac{\beta_1 E+\beta_2 I}{N}\right)d\tau}(\pi+\theta R)\,d\tau.$$

$$S(t) = e^{-\int_0^t\left(\mu+\frac{\beta_1 E+\beta_2 I}{N}\right)d\tau}\left[S(0) + \int_0^t e^{\int_0^t\left(\mu+\frac{\beta_1 E+\beta_2 I}{N}\right)d\tau}(\pi+\theta R)\,d\tau\right] > 0.$$

Similarly, it can be shown that $E(t) > 0, I(t) > 0, Q(t) > 0$ and $R(t) > 0$. Thus, the solutions $S(t), E(t), I(t), Q(t), R(t)$ of *Systems (1)-(5)* remains positive for all $t > 0$. If $S(t), E(t), I(t), Q(t)$ and $R(t)$ are non-negative, then $N(t) = S(t) + E(t) + I(t) + Q(t) + R(t) > 0$.

2.1.3 | Equilibrium points of the model

The equilibrium points of the model system are obtained by setting the right-hand side of the differential equations equal to zero and solving each to get a constant solution. Epidemiological models usually have two equilibrium points, namely, a disease-free equilibrium point and an endemic equilibrium point.

2.1.4 | Disease free equilibrium point (DFEP)

The disease-free equilibrium of the model, *Eqs. (1)-(5)*, is obtained by making $\frac{dS}{dt} = \frac{dE}{dt} = \frac{dI}{dt} = \frac{dQ}{dt} = \frac{dR}{dt} = 0$. Further, at the disease-free equilibrium point, there is no infectious person of the disease in the population, i.e. $E = I = Q = 0$. Therefore, the disease-free equilibrium point is given by

$$X_0 = \left(\frac{\pi}{\mu}, 0,0,0,0\right).$$

The point X_0 is a non-negative equilibrium, which exists without any condition. This equilibrium implies that in the absence of any infection, the total population size remains at its equilibrium value $\frac{\pi}{\mu}$.

2.1.5 | Endemic equilibrium point (EEP)

The endemic equilibrium point of the model, *Eqs. (1)-(5)*, is obtained by making $\frac{dS}{dt} = \frac{dE}{dt} = \frac{dI}{dt} = \frac{dQ}{dt} = \frac{dR}{dt} = 0$. From the model we have

$$\frac{dS}{dt} = \pi + \theta R - \mu S - \frac{\beta_1 SE + \beta_2 SI}{N} = 0. \quad (6)$$

$$\frac{dE}{dt} = \frac{\beta_1 SE + \beta_2 SI}{N} - (\mu+\sigma)E = 0. \quad (7)$$

$$\frac{dI}{dt} = \delta\sigma E - (\mu+\alpha_1+\omega)I = 0. \quad (8)$$

$$\frac{dQ}{dt} = \omega I - (\mu+\alpha_2+\gamma)Q = 0. \quad (9)$$

$$\frac{dR}{dt} = (1-\delta)\sigma E + \gamma Q - (\mu+\theta)R = 0. \quad (10)$$

From *Eq. (8)*, $\delta\sigma E - (\mu+\alpha_1+\omega)I = 0$ we get

$$E = \frac{(\mu+\alpha_1+\omega)I}{\delta\sigma}. \quad (11)$$

From *Eq. (9)*, $\omega I - (\mu+\alpha_2+\gamma)Q = 0$ we get

$$Q = \frac{\omega I}{\mu + \alpha_2 + \gamma}. \tag{12}$$

From *Eq. (10)*, $(1-\delta)\sigma E + \gamma Q - (\mu+\theta)R = 0$ we get

$$R = \frac{(1-\delta)\sigma E + \gamma Q}{\mu + \theta}.$$

Substituting the value of $E = \frac{(\mu+\alpha_1+\omega)I}{\delta\sigma}$ and $Q = \frac{\omega I}{\mu+\alpha_2+\gamma}$ into the equation $R = \frac{(1-\delta)\sigma E+\gamma Q}{\mu+\theta}$ implies

$$R = \left[\frac{(1-\delta)(\mu+\alpha_1+\omega)}{\delta(\mu+\theta)} + \frac{\gamma\omega}{(\mu+\alpha_2+\gamma)(\mu+\theta)}\right] I. \tag{13}$$

From *Eq. (7)*, $\frac{\beta_1 SE+\beta_2 SI}{N} - (\mu+\sigma)E = 0$ we get

$$S = \frac{(\mu+\sigma)EN}{\beta_1 E + \beta_2 I}.$$

Substituting the value of $E = \frac{(\mu+\alpha_1+\omega)I}{\delta\sigma}$ into the equation $S = \frac{(\mu+\sigma)EN}{\beta_1 E+\beta_2 I}$ implies

$$S = \frac{(\mu+\sigma)(\mu+\alpha_1+\omega)N}{\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2}. \tag{14}$$

From *Eq. (6)*, $\pi + \theta R - \mu S - \frac{\beta_1 SE+\beta_2 SI}{N} = 0$, we get. Substituting the value of E, R and S into the equation $\pi + \theta R - \mu S - \frac{\beta_1 SE+\beta_2 SI}{N} = 0$ implies

$$\pi + \theta\left[\frac{(1-\delta)(\mu+\alpha_1+\omega)}{\delta(\mu+\theta)} + \frac{\gamma\omega}{(\mu+\alpha_2+\gamma)(\mu+\theta)}\right] I - \frac{\mu(\mu+\sigma)(\mu+\alpha_1+\omega)N}{\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2}$$
$$- \frac{\beta_1\left(\frac{(\mu+\sigma)(\mu+\alpha_1+\omega)N}{\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2}\right)\left(\frac{(\mu+\alpha_1+\omega)I}{\delta\sigma}\right) + \beta_2\left(\frac{(\mu+\sigma)(\mu+\alpha_1+\omega)N}{\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2}\right) I}{N} = 0,$$

$$\pi + \left[\frac{(1-\delta)\theta(\mu+\alpha_1+\omega)}{\delta(\mu+\theta)} + \frac{\theta\gamma\omega}{(\mu+\alpha_2+\gamma)(\mu+\theta)}\right] I - \frac{\mu(\mu+\sigma)(\mu+\alpha_1+\omega)N}{\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2}$$
$$- \beta_1\left(\frac{(\mu+\sigma)(\mu+\alpha_1+\omega)N}{\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2}\right)\left(\frac{(\mu+\alpha_1+\omega)}{\delta\sigma}\right) I$$
$$- \beta_2\left(\frac{(\mu+\sigma)(\mu+\alpha_1+\omega)N}{\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2}\right) I = 0, \tag{15}$$

$$\left[\frac{(1-\delta)\theta(\mu+\alpha_1+\omega)}{\delta(\mu+\theta)} + \frac{\theta\gamma\omega}{(\mu+\alpha_2+\gamma)(\mu+\theta)}\right] I - \frac{\beta_1(\mu+\alpha_1+\omega)(\mu+\sigma)(\mu+\alpha_1+\omega)N}{\delta\sigma(\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2)} I$$
$$- \frac{\beta_2(\mu+\sigma)(\mu+\alpha_1+\omega)N}{\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2} I = \frac{\mu(\mu+\sigma)(\mu+\alpha_1+\omega)N}{\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2} - \pi$$

$$\left[\frac{(1-\delta)\theta(\mu+\alpha_1+\omega)(\mu+\alpha_2+\gamma)+\delta\theta\gamma\omega}{\delta(\mu+\theta)(\mu+\alpha_2+\gamma)}\right] I$$
$$- \frac{\beta_1(\mu+\alpha_1+\omega)(\mu+\sigma)(\mu+\alpha_1+\omega)N + \delta\sigma\beta_2(\mu+\sigma)(\mu+\alpha_1+\omega)N}{\delta\sigma(\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2)} I$$
$$= \frac{\mu(\mu+\sigma)(\mu+\alpha_1+\omega)N}{\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2} - \pi$$

$$\left[\frac{\begin{matrix}[(1-\delta)\theta(\mu+\alpha_1+\omega)(\mu+\alpha_2+\gamma)+\delta\theta\gamma\omega]\sigma(\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2)- \\ \left[\begin{matrix}\beta_1(\mu+\alpha_1+\omega)(\mu+\sigma)(\mu+\alpha_1+\omega)N \\ +\delta\sigma\beta_2(\mu+\sigma)(\mu+\alpha_1+\omega)N\end{matrix}\right](\mu+\theta)(\mu+\alpha_2+\gamma)\end{matrix}}{\delta\sigma(\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2)(\mu+\theta)(\mu+\alpha_2+\gamma)}\right]I$$

$$=\frac{\mu(\mu+\sigma)(\mu+\alpha_1+\omega)N}{\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2}-\pi,$$

$$I=\frac{A[\mu(\mu+\sigma)(\mu+\alpha_1+\omega)N-\pi(\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2)]}{[\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2][K-M(\mu+\theta)(\mu+\alpha_2+\gamma)]},$$

where $A=\delta\sigma(\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2)(\mu+\theta)(\mu+\alpha_2+\gamma)$,

$K=[(1-\delta)\theta(\mu+\alpha_1+\omega)(\mu+\alpha_2+\gamma)+\delta\theta\gamma\omega]\sigma(\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2)$ and
$M=\beta_1(\mu+\alpha_1+\omega)(\mu+\sigma)(\mu+\alpha_1+\omega)N+\delta\sigma\beta_2(\mu+\sigma)(\mu+\alpha_1+\omega)N$.

Therefore, the Endemic Equilibrium Point (EEP) denoted by $X^*$of the model in *Eqs. (1)-(5)* is given by

$$X^*=(S^*,E^*,I^*,Q^*,R^*),$$

where $S^*=\frac{(\mu+\sigma)(\mu+\alpha_1+\omega)N}{\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2}$, $E^*=\frac{(\mu+\alpha_1+\omega)I^*}{\delta\sigma}$.

$$I^*=\frac{\delta\sigma(\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2)(\mu+\theta)(\mu+\alpha_2+\gamma)}{[\mu(\mu+\sigma)(\mu+\alpha_1+\omega)N-\pi(\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2)]}{[\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2][K-M(\mu+\theta)(\mu+\alpha_2+\gamma)]}.$$

$$Q^*=\frac{\omega I^*}{\mu+\alpha_2+\gamma}\quad\text{and}\quad R^*=\left[\frac{(1-\delta)\sigma(\mu+\alpha_1+\omega)}{\delta\sigma(\mu+\theta)}+\frac{\gamma\omega}{(\mu+\alpha_2+\gamma)(\mu+\theta)}\right]I^*.$$

$K=[(1-\delta)\theta(\mu+\alpha_1+\omega)(\mu+\alpha_2+\gamma)+\delta\theta\gamma\omega]\sigma(\beta_1(\mu+\alpha_1+\omega)+\delta\sigma\beta_2)$ and
$M=\beta_1(\mu+\alpha_1+\omega)(\mu+\sigma)(\mu+\alpha_1+\omega)N+\delta\sigma\beta_2(\mu+\sigma)(\mu+\alpha_1+\omega)N$

2.1.6 | The basic reproduction number

The primary reproduction number is usually denoted as R_0 defines the average number of secondary infections caused by an individual in an entirely susceptible population. The value of R_0will indicate whether the epidemic could occur or not. If $R_0<1$, then the disease will decrease and eventually die out. If $R_0=1$, each existing infection causes one new infection. The disease will stay alive and stable, but there will not be an outbreak or an epidemic. If $R_0>1$, each existing infection causes more than one new infection. The disease will spread between people, and there may be an outbreak or epidemic. To find the reproduction number, we will use the method of the next-generation matrix [12], defined as the model's spectral radius (or dominant eigenvalue). The first step is rewriting the model equations, starting with newly infective classes:

$$\frac{dE}{dt}=\frac{\beta_1SE+\beta_2SI}{N}-(\mu+\sigma)E,$$
$$\frac{dI}{dt}=\delta\sigma E-(\mu+\alpha_1+\omega)I,$$
$$\frac{dQ}{dt}=\omega I-(\mu+\alpha_2+\gamma)Q.$$

Setting $x=(E,I,Q,R,S)^T$, then *System (1)* can be written as

$$\frac{dx}{dt}=f(x)-v(x).$$

Here, the new infection matrix $f(x)$ and the transition matrix $v(x)$ are defined by

$$f(x) = \begin{pmatrix} \frac{\beta_1 SE + \beta_2 SI}{N} \\ 0 \\ 0 \end{pmatrix} \text{ and } v(x) = \begin{pmatrix} (\mu+\sigma)E \\ (\mu+\alpha_1+\omega)I - \delta\sigma E \\ (\mu+\alpha_2+\gamma)Q - \omega I \end{pmatrix}.$$

Then, by the principle of next-generation matrix, the Jacobian matrices at DFE are given by

$$V^{-1} = \begin{pmatrix} \frac{1}{\mu+\sigma} & 0 & 0 \\ \frac{\delta\sigma}{(\mu+\sigma)(\mu+\alpha_1+\omega)} & \frac{1}{\mu+\alpha_1+\omega} & 0 \\ \frac{\delta\sigma\omega}{(\mu+\sigma)(\mu+\alpha_1+\omega)(\mu+\alpha_2+\gamma)} & \frac{\omega}{(\mu+\alpha_1+\omega)(\mu+\alpha_2+\gamma)} & \frac{1}{\mu+\alpha_2+\gamma} \end{pmatrix},$$

$$FV^{-1} = \begin{pmatrix} \frac{\beta_1(\mu+\alpha_1+\omega)+\beta_2\delta\sigma}{(\mu+\sigma)(\mu+\alpha_1+\omega)} & \frac{\beta_2}{(\mu+\alpha_1+\omega)} & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}.$$

Therefore, FV^{-1} is the next-generation matrix of the SEIQR model. The dominant eigenvalue of FV^{-1} represents $R_0 = \rho(FV^{-1})$, which is

$$R_0 = \frac{\beta_1(\mu+\alpha_1+\omega)+\beta_2\delta\sigma}{(\mu+\sigma)(\mu+\alpha_1+\omega)}. \quad \textbf{(16)}$$

3 | Stability Analysis of Diseases-Free Equilibrium

Theorem 2. The disease-free equilibrium point X_0 of the dynamical *Systems (1)-(5)* is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.

Proof: the Jacobian matrix at any equilibrium point $X = (S, E, I, Q, R)$ is given by

$$J(X) = \begin{bmatrix} \frac{-\beta_1 E - \beta_2 I}{N} - \mu & \frac{-\beta_1 S}{N} & \frac{-\beta_2 S}{N} & 0 & \theta \\ \frac{\beta_1 E + \beta_2 I}{N} & \frac{\beta_1 S}{N} - (\mu+\sigma) & \frac{\beta_2 S}{N} & 0 & 0 \\ 0 & \delta\sigma & -(\mu+\alpha_1+\omega) & -(\mu+\alpha_2+\gamma) & \sigma \\ 0 & 0 & \omega & \gamma & -(\mu+\theta) \\ 0 & (1-\delta)\sigma & 0 & & \end{bmatrix}.$$

The Jacobian matrix at the disease-free equilibrium point $X_0 = \left(\frac{\pi}{\mu}, 0,0,0,0\right)$ is given by

$$J(X_0) = \begin{bmatrix} -\mu & -\beta_1 & -\beta_2 & 0 & \theta \\ 0 & \beta_1 - (\mu+\sigma) & \beta_2 & 0 & 0 \\ 0 & \delta\sigma & -(\mu+\alpha_1+\omega) & 0 & 0 \\ 0 & 0 & \omega & -(\mu+\alpha_2+\gamma) & \sigma \\ 0 & (1-\delta)\sigma & 0 & \gamma & -(\mu+\theta) \end{bmatrix}.$$

The characteristic equation of this matrix is given by $\det(J(X_0) - \lambda I_5) = 0$, where I_5 is a square identity matrix of order 5, and λ is the eigenvalues of the Jacobian matrix. Therefore, the characteristic equation is $(\mu+\lambda)\big[\lambda^4 + (4\mu+\alpha_1+\omega+\sigma+\theta+\alpha_2+\gamma-\beta_1)\lambda^3 + \big[(2\mu+\alpha_1+\omega+\sigma-\beta_1)(2\mu+\theta+\alpha_2+\gamma) + (\mu+\alpha_2+\gamma)(\mu+\theta) - \big[\big(\beta_1-(\mu+\sigma)\big)(\mu+\alpha_1+\omega)+\beta_2\delta\sigma\big] + \sigma\gamma\big]\lambda^2 + \big[(\mu+\alpha_2+\gamma)(\mu+\theta)(2\mu+\alpha_1+\omega+\sigma-\beta_1) - (2\mu+\theta+\alpha_2+\gamma)\big[\big(\beta_1-(\mu+\sigma)\big)(\mu+\alpha_1+\omega)+\beta_2\delta\sigma\big] + \sigma\gamma(\mu+\alpha_1+\omega+\mu+\sigma-\beta_1)\big]\lambda - \sigma\gamma\big[\big(\beta_1-(\mu+\sigma)\big)(\mu+\alpha_1+\omega)+\beta_2\delta\sigma\big] - (\mu+\alpha_2+\gamma)(\mu+\theta)\big[\big(\beta_1-(\mu+\sigma)\big)(\mu+\alpha_1+\omega)+\beta_2\delta\sigma\big]\big] = 0.$

The Jacobian evaluated at the DFE has five eigenvalues, one of which is $\lambda_1 = -\mu$, which is negative.

The remaining four are eigenvalues of the roots of the equation given by

$$a_4\lambda^4 + a_3\lambda^3 + a_2\lambda^2 + a_1\lambda + a_0 = 0,$$

where

$$a_4 = 1,\ a_3 = 4\mu + \alpha_1 + \omega + \sigma + \theta + \alpha_2 + \gamma - \beta_1,$$
$$a_2 = \big[(2\mu + \alpha_1 + \omega + \sigma - \beta_1)(2\mu + \theta + \alpha_2 + \gamma) + (\mu + \alpha_2 + \gamma)(\mu + \theta) -$$
$$\big[\big(\beta_1 - (\mu + \sigma)\big)(\mu + \alpha_1 + \omega) + \beta_2\delta\sigma\big] + \sigma\gamma\big],$$
$$a_1 = \big[(\mu + \alpha_2 + \gamma)(\mu + \theta)(2\mu + \alpha_1 + \omega + \sigma - \beta_1) - (2\mu + \theta + \alpha_2 + \gamma)\big[\big(\beta_1 -$$
$$(\mu + \sigma)\big)(\mu + \alpha_1 + \omega) + \beta_2\delta\sigma\big] + \sigma\gamma(2\mu + \alpha_1 + \omega + \sigma - \beta_1)\big],$$
$$a_0 = -\sigma\gamma\big[\big(\beta_1 - (\mu + \sigma)\big)(\mu + \alpha_1 + \omega) + \beta_2\delta\sigma\big] - (\mu + \alpha_2 + \gamma)(\mu + \theta)\big[\big(\beta_1 -$$
$$(\mu + \sigma)\big)(\mu + \alpha_1 + \omega) + \beta_2\delta\sigma\big].$$

By Routh-Hurwitz criteria, the DFE equilibrium X_0 is local asymptotically stable if $a_0 > 0, a_1 > 0, a_2 > 0, a_3 > 0, a_3a_2 - a_1 > 0$ and $a_3a_2a_1 - {a_1}^2 - a_0{a_3}^2 > 0$.

4 | Stability Analysis of Endemic Equilibrium Point

Theorem 3. The endemic equilibrium point X^* of the *Dynamical System (1)-(5)* is locally asymptotically stable if $R_0 > 1$ and unstable if $R_0 < 1$.

Proof: the Jacobian matrix at the endemic equilibrium point $X^* = (S^*, E^*, I^*, Q^*, R^*)$ is given by

$$J(X^*) = \begin{bmatrix} k_1 & k_2 & k_3 & 0 & \theta \\ k_4 & k_5 & k_6 & 0 & 0 \\ 0 & \delta\sigma & -(\mu + \alpha_1 + \omega) & 0 & 0 \\ 0 & 0 & \omega & -(\mu + \alpha_2 + \gamma) & \sigma \\ 0 & (1-\delta)\sigma & 0 & \gamma & -(\mu + \theta) \end{bmatrix}.$$

$k_1 = \frac{-\beta_1 E^* - \beta_2 I^*}{N} - \mu$, $k_2 = \frac{-\beta_1 S^*}{N}$, $k_3 = \frac{-\beta_2 S^*}{N}$, $k_4 = \frac{\beta_1 E^* + \beta_2 I^*}{N}$, $k_5 = \frac{\beta_1 S^*}{N} - (\mu + \sigma)$ and $k_6 = \frac{\beta_2 S^*}{N}$.

The characteristic equation of this matrix is given by $\det(J(X^*) - \lambda I_5) = 0$, where I_5 is a square identity matrix of order 5, and λ is the eigenvalue of the Jacobian matrix. Therefore, the characteristic equation is

$$a_5\lambda^5 + a_4\lambda^4 + a_3\lambda^3 + a_2\lambda^2 + a_1\lambda + a_0 = 0,$$

where

$$a_5 = 1,$$
$$a_4 = 3\mu + \alpha_1 + \alpha_2 + \gamma + \theta + \omega - k_5 - k_1,$$
$$a_3 = (2\mu + \alpha_2 + \gamma + \theta)(\mu + \alpha_1 + \omega - k_5) + (\mu + \alpha_2 + \gamma)(\mu + \theta) + k_4k_2 -$$
$$[(\mu + \alpha_1 + \omega)k_5 + k_6\delta\sigma] - \sigma\gamma - k_1(3\mu + \alpha_1 + \alpha_2 + \gamma + \theta + \omega - k_5),$$
$$a_2 = (\mu + \alpha_2 + \gamma)(\mu + \theta)(\mu + \alpha_1 + \omega - k_5) + k_4[(\mu + \alpha_1 + \omega + k_3\delta\sigma)k_2 + (\mu + \theta)k_2 +$$
$$\theta(1-\delta)\sigma + (\mu + \alpha_2 + \gamma)k_2] - (2\mu + \alpha_2 + \gamma + \theta)[(\mu + \alpha_1 + \omega)k_5 + k_6\delta\sigma] -$$
$$\sigma\gamma(\mu + \alpha_1 + \omega - k_5) - k_1[(2\mu + \alpha_2 + \gamma + \theta)(\mu + \alpha_1 + \omega - k_5) + (\mu + \alpha_2 + \gamma)(\mu + \theta) -$$
$$[(\mu + \alpha_1 + \omega)k_5 + k_6\delta\sigma] - \delta\gamma],$$
$$a_1 = k_4[(\mu + \theta)(\mu + \alpha_1 + \omega + k_3\delta\sigma)k_2 + \theta(1-\delta)\sigma(\mu + \alpha_1 + \omega) + (\mu + \alpha_2 +$$
$$\gamma)[(\mu + \alpha_1 + \omega + k_3\delta\sigma)k_2) + (\mu + \theta)k_2 + \theta(1-\delta)\sigma] - \gamma k_2\sigma] + (\mu + \alpha_1 + \omega)\gamma k_5\sigma +$$
$$\gamma k_6\delta\sigma^2 - k_1[(\mu + \alpha_2 + \gamma)(\mu + \theta)(\mu + \alpha_1 + \omega - k_5) - (2\mu + \alpha_2 + \gamma + \theta)[(\mu + \alpha_1 +$$
$$\omega)k_5 + k_6\delta\sigma] - \sigma\gamma(\mu + \alpha_1 + \omega - k_5)] - (\mu + \alpha_2 + \gamma)(\mu + \theta)[(\mu + \alpha_1 + \omega)k_5 + k_6\delta\sigma],$$
$$a_0 = k_1(\mu + \alpha_2 + \gamma)(\mu + \theta)[(\mu + \alpha_1 + \omega)k_5 + k_6\delta\sigma] - (\mu + \alpha_1 + \omega)\gamma k_5k_1\sigma +$$
$$\gamma k_1k_6\delta\sigma^2 - k_4\gamma k_2\sigma(\mu + \alpha_1 + \omega) - k_4\gamma\delta\sigma(k_3\sigma - \theta\omega) + k_4(\mu + \alpha_2 + \gamma)[(\mu + \theta)(\mu +$$
$$\alpha_1 + \omega + k_3\delta\sigma)k_2 + \theta(1-\delta)\sigma(\mu + \alpha_1 + \omega)].$$

By Routh-Hurwitz criteria, the endemic equilibrium X^* is locally asymptotically stable if $a_4 > 0, \frac{a_3a_4 - a_2}{a_4} > 0, a_2 - \frac{a_1a_4^2 - a_0a_4}{a_3a_4 - a_2} > 0, \frac{a_1a_4 - a_0}{a_4} - \frac{(a_0a_3a_4 - a_0a_2)(a_3a_4 - a_2)}{a_4(a_2a_3a_4 - a_2^2 - a_1a_4^2 + a_0a_4)} > 0$ and $a_0 > 0$.

5 | Parameter Estimation for Numerical Simulation

To perform numerical simulation, we collect the following parameter values obtained from different sources.

Table 1. Parameter estimation.

Parameter Symbol	Value	Source
N	2000	Assumed
π	100	[3]
β_1	0.045	Assumed
β_2	0.04	Assumed
μ	0.016	[8]
θ	0.15	[8]
σ	0.07	[8]
δ	0.7	[8]
ω	0.024	[3]
α_1	0.001	[3]
α_2	0.004	[3]
γ	0.015	[3]

Therefore, the basic reproduction number (R_0) of the model is equal to

$$R_0 = \frac{\beta_1(\mu+\alpha_1+\omega)+\beta_2\delta\sigma}{(\mu+\sigma)(\mu+\alpha_1+\omega)} = 1.07912.$$

6 | Numerical Analysis

The numerical analysis is obtained from the graphs of basic reproduction numbers concerning the parameters obtained and given in *Table 1*.

Let us take our control parameter to be β_1

The basic control parameters that can decrease the spread of the disease is β_1 which is the transmission coefficient from susceptible individuals to exposed individuals due to the movement and contact between them. The graphical representation of the control parameter $\beta_1$vs the basic reproduction number R_0 is given below:

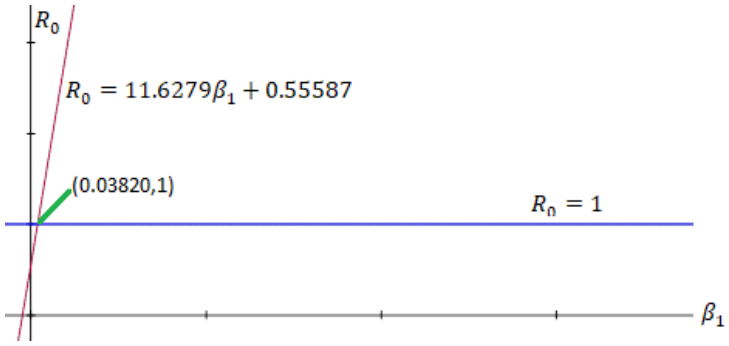

Fig. 1. This figure shows the impact of the control parameter β_1 on the basic reproduction number R_0.

To control the spread of COVID-19, the numerical value of the control parameter β_1 never greater than 0.03820.

Let us take our control parameter to be β_2

The basic control parameters that can decrease the spread of the disease is β_2 which is the transmission coefficient from susceptible individuals to infected individuals with symptoms and carriers of the virus due to the movement and contact that occur among them. The graphical representation of the control parameter $\beta_2$vs the basic reproduction number R_0 is given below:

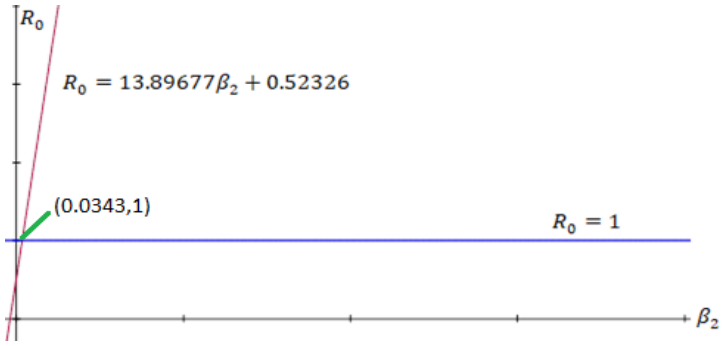

Fig. 2. This figure shows the impact of the control parameter β_2 on the basic reproduction number R_0.

To control the spread of COVID-19, the numerical value of the control parameter β_2 never greater than 0.0343.

Let us take our control parameter to be σ

The basic control parameter that can decrease the spread of the disease is σ, which is the progression rate from E to either I or R. The graphical representation of the control parameter σ vs, the basic reproduction number R_0 is given below:

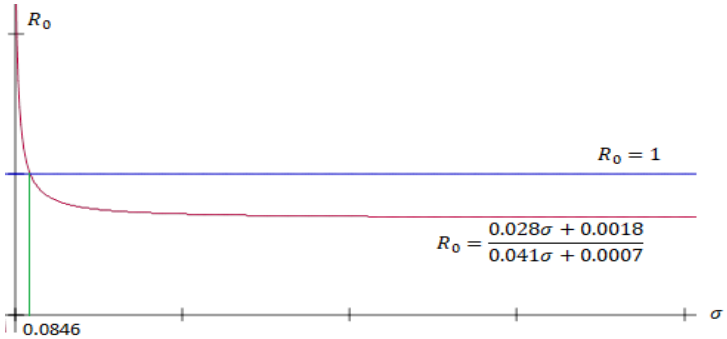

Fig. 3. This figure shows the impact of the control parameter σ on the basic reproduction number R_0.

To control the spread of COVID-19, the numerical value of the control parameter σ never less than 0.0846.

Let us take our control parameter to be ω

The basic control parameter that can decrease the spread of the disease is ω which is the transmission coefficient of the infected people with symptoms and carriers of the virus to the quarantined infected (hospitalized cases). The graphical representation of the control parameter ω vs, the basic reproduction number R_0 is given below:

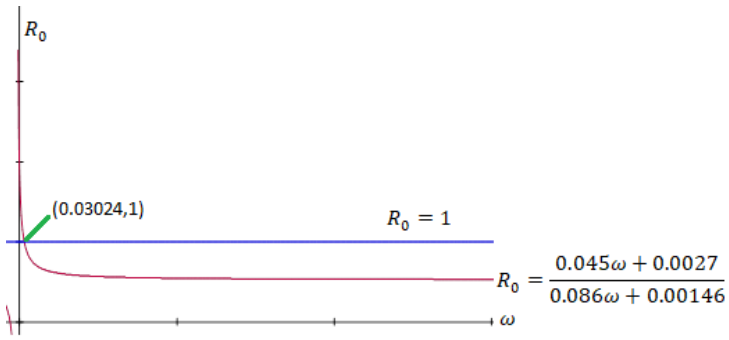

Fig. 4. This figure shows the impact of the control parameter ω on the basic reproduction number R_0.

To control the spread of COVID-19, the numerical value of the control parameter ω never less than 0.03024.

Let us take our control parameter to be α_1

The basic control parameters that can decrease the spread of the disease is α_1, which is the death rate of the Infected population due to Covid-19 infection. The graphical representation of the control parameter α_1 vs the basic reproduction number R_0 is given below:

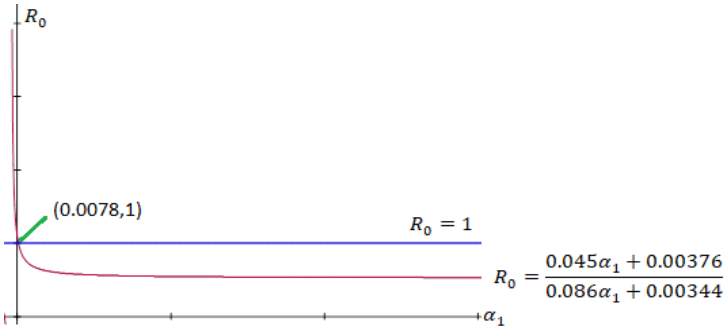

Fig. 5. This figure shows the impact of the control parameter α_1 on the basic reproduction number R_0.

To control the spread of COVID-19, the numerical value of the control parameter α_1 never less than 0.0078.

Let us take our control parameter to be μ

The basic control parameter that can decrease the spread of the disease is μ, which is the natural death rate. The graphical representation of the control parameter μ vs, the basic reproduction number R_0 is given below;

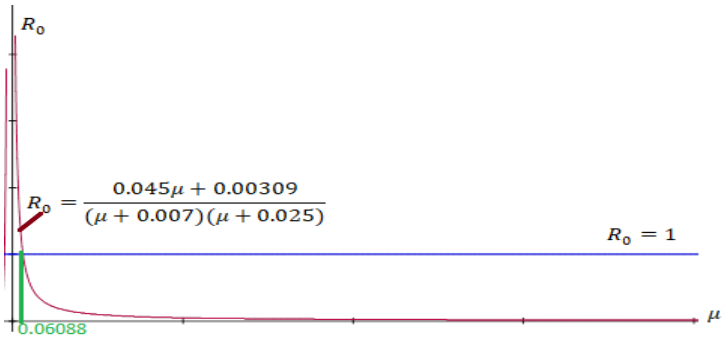

Fig. 6. This figure shows the impact of the control parameter μ on the basic reproduction number R_0.

If the natural death rate μ between 0 and 0.06088, then the reproduction number decreases, with $R_0 > 1$ and this tells us the disease still persists. If the natural death rate is greater than 0.06088, then the reproduction number decreases, with $R_0 < 1$, and this tells us the disease dies out.

7 | Sensitivity Analysis

In determining how best to reduce human mortality and morbidity due to COVID-19, it is necessary to know the relative importance of the factors responsible for its transmission. Sensitivity analysis is commonly used to determine the robustness of model predictions to parameter values, that is, to help us know the parameters that have a high impact on the reproduction number R_0 (because there are usually errors in data collection and presumed parameter values). For sensitivity analysis, we use the normalized sensitivity index [13]. The normalized forward sensitivity indices of R_0 that depends differentiable on a parameter m, is defined by $H_m^{R_0} = \frac{m}{R_0}\frac{\partial R_0}{\partial m}$, we take $m = \beta_1, \beta_2, \sigma, \alpha_1, \omega$ and μ. The sensitivity indices of R_0 with respect to m is given as

$$H_{\beta_1}^{R_0} = \frac{\beta_1(\mu+\alpha_1+\omega)}{\beta_1(\mu+\alpha_1+\omega)+\beta_2\delta\sigma},$$
$$H_{\beta_2}^{R_0} = \frac{\beta_2\delta\sigma}{\beta_1(\mu+\alpha_1+\omega)+\beta_2\delta\sigma},$$
$$H_{\sigma}^{R_0} = \frac{-\beta_1\sigma(\mu+\alpha_1+\omega)+\beta_2\sigma\delta(\mu+\sigma)-\beta_2\delta\sigma^2}{(\mu+\sigma)[\beta_1(\mu+\alpha_1+\omega)+\beta_2\delta\sigma]},$$
$$H_{\alpha_1}^{R_0} = \frac{-\alpha_1\beta_2\delta\sigma}{(\mu+\alpha_1+\omega)[\beta_1(\mu+\alpha_1+\omega)+\beta_2\delta\sigma]},$$
$$H_{\omega}^{R_0} = \frac{-\omega\beta_2\delta\sigma}{(\mu+\alpha_1+\omega)[\beta_1(\mu+\alpha_1+\omega)+\beta_2\delta\sigma]},$$
$$H_{\mu}^{R_0} = \frac{\beta_1\mu(\mu+\sigma)(\mu+\alpha_1+\omega)-\mu[\beta_1(\mu+\alpha_1+\omega)+\beta_2\delta\sigma](2\mu+\alpha_1+\omega+\sigma)}{(\mu+\sigma)(\mu+\alpha_1+\omega)[\beta_1(\mu+\alpha_1+\omega)+\beta_2\delta\sigma]}.$$

After some simplifications and numerical calculation, we get values of the sensitivity index for the critical parameters mentioned in *Table 2*.

Table 2. Numerical values of sensitivity indices of R_0.

Parameter Symbol	Sensitivity Index
β_2	0.5151
β_1	0.4849
μ	-0.3871
ω	-0.3015
σ	-0.2345
α_1	-0.0013

The parameters given in *Table 2* are ordered from the most sensitive to the least sensitive. The parameter values $\beta_1 = 0.045, \beta_2 = 0.04, \mu = 0.016, \delta = 0.7, \sigma = 0.07$, $\alpha_1 = 0.001$ and $\omega = 0.024$ are used to determine the sensitivity indices.

From the sensitivity indices of R_0 above, generally, it shows that when the parameter values β_1 and β_2 increase while the other parameters remain constant, the value of R_0 increase, implying that they increase the endemicity of the disease as they have positive indices. When the parameters ω, μ, α_1, and σ increase the other parameters remain constant the value of R_0 decrease implying that they decrease the endemicity of the disease as they have negative indices.

The most sensitive parameters are β_2 (the transmission coefficient from susceptible individuals to infected individuals with symptoms and carriers of the virus due to the movement and contact that occur among them) and β_1 (the transmission coefficient from susceptible individuals to exposed individuals with symptoms and carriers of the virus due to the movement and contact that occur among them) and the least sensitive parameter is the death rate of the infected population due to Covid-19 infection α_1.

8 | Conclusion

In this study, a deterministic model for the dynamics of COVID-19 is presented and analyzed. The disease-free and endemic equilibrium was obtained, and their stabilities were investigated. The basic reproduction number (R_0) was computed using the next-generation matrix method. The model showed that the disease-free equilibrium is unstable when $R_0 > 1$ that means that the disease will persist. We also studied the sensitivity analysis of model parameters to know the parameters that have a high impact on the reproduction number R_0.

From the above numerical simulation, we would like to recommend the following to control the spread of COVID-19: To control the spread of COVID-19, we investigate the five most influential control parameters to make the basic reproduction number R_0 to be less than one. The numerical value of the control parameter β_1 (the transmission coefficient from susceptible individuals to expose individuals due to the movement and contact that occur among them) never exceed 0.0382, the numerical value of the control parameter β_2 (the transmission coefficient from susceptible individuals to infected individuals with symptoms and carriers of

the virus due to the movement and contact that occur among them) never exceed 0.0343, the numerical value of the control parameter σ (the progression rate from E to either I or R) never less than 0.0846, the numerical value of the control parameter ω (the transmission coefficient of the infected people with symptoms and carriers of the virus to the quarantined infected) never less than 0.3024, the numerical value of the control parameter α_1(the death rate of the Infected population due to Covid-19 infection) never less than 0.0078.

Author Contributions

Mengesha Dibru Firdawoke: Conceptualized the study, developed the mathematical model, and performed the stability analysis.

Mekash Ayalew Mohammed: Conducted the numerical simulations, interpreted the results, and contributed to the sensitivity analysis.

Eshetu Dadi Gurmu: Compiled and reviewed the literature, drafted the manuscript, and coordinated revisions.

Data Availability Statement

The datasets used and/or analyzed during the current study are available from the corresponding author upon reasonable request.

Conflict of Interest

The authors declare that there are no conflicts of interest regarding the publication of this paper.

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